RAW SEQUENCE LISTING
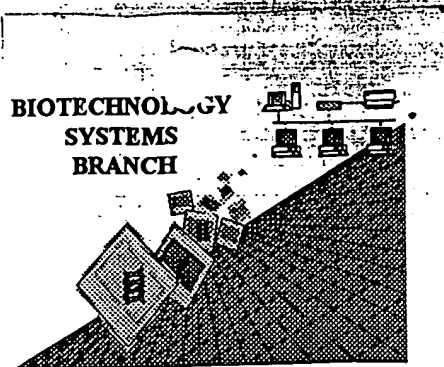# ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/524,531_

Source: _1646_

Date Processed by STIC: _7/28/2000_

THE ATTACHED PRIN~ ~~ ~INS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,

2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE __CHECKER VERSION 3.0 PROGRAM__, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

R● Sequence Listing Error S   mary

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TECH CENTER 1600/2900

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.**

8 _____ Skipped Sequences
(OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences
(NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's
(NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism
(NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature
(NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol..63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

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AUG 08 2000

1646

```
RAW SEQUENCE LISTING              DATE: 07/28/2000
PATENT APPLICATION: US/09/524,531 TIME: 13:29:08
```

Does Not Comply
Corrected Diskette Needed

```
Input Set : A:\imhof.app.txt
Output Set: N:\CRF3\07282000\I524531.raw
```

```
  3 <110> APPLICANT: RMF Dictagene S.A.
  5 <120> TITLE OF INVENTION: Vascular adhesion molecules and modulation of their
  6       function
  8 <130> FILE REFERENCE: rmf6usseqlist
 10 <140> CURRENT APPLICATION NUMBER: 09/524531
 11 <141> CURRENT FILING DATE: 2000-03-13
 13 <150> PRIOR APPLICATION NUMBER: EP 99.200746.8
 14 <151> PRIOR FILING DATE: 1999-03-11
 16 <160> NUMBER OF SEQ ID NOS: 21
 18 <170> SOFTWARE: PatentIn Ver. 2.1
```

ERRORED SEQUENCES

```
550 <210> SEQ ID NO: 21
551 <211> LENGTH: 300
552 <212> TYPE: PRT
553 <213> ORGANISM: Mus musculus
555 <400> SEQUENCE: 21
556 Met Gly Thr Glu Gly Lys Ala Gly Arg Lys Leu Leu Phe Leu Phe Thr
557  1               5                  10                  15
559 Ser Met Ile Leu Gly Ser Leu Val Gln Gly Lys Gly Ser Val Tyr Thr
560              20                  25                  30
562 Ala Gln Ser Asp Val Gln Val Pro Glu Met Glu Ser Ile Lys Leu Thr
563          35                  40                  45
565 Cys Thr Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe Val
566      50                  55                  60
568 Gln Gly Ser Thr Thr Ala Leu Val Cys Tyr Asn Ser Gln Ile Thr Ala
569  65                  70                  75                  80
571 Pro Tyr Ala Asp Arg Val Thr Phe Ser Ser Glu Gly Ile Thr Phe Ser
572              85                  90                  95
574 Ser Val Thr Arg Lys Asp Asn Gly Glu Tyr Thr Cys Met Val Ser Glu
575             100                 105                 110
577 Glu Gly Gly Gln Asn Tyr Gly Glu Val Ser Ile His Leu Thr Val Leu
578             115                 120                 125
580 Val Pro Pro Ser Lys Pro Thr Ile Ser Val Pro Ser Ser Val Thr Ile
581         130                 135                 140
583 Gly Asn Arg Ala Val Leu Thr Cys Ser Glu His Asp Gly Ser Pro Pro
584 145                 150                 155                 160
586 Ser Glu Tyr Ser Trp Phe Lys Asp Gly Ile Ser Met Leu Thr Ala Asp
587                 165                 170                 175
589 Ala Lys Lys Thr Arg Ala Phe His Asn Ser Ser Phe Thr Ile Asp Pro
590             180                 185                 190
592 Lys Ser Gly Asp Leu Tyr Phe Asp Phe Val Thr Ala Phe Asp Ser Gly
593         195                 200                 205
595 Glu Tyr Tyr Cys Gln Ala Gln Asn Gly Tyr Gly Thr Ala Met Arg Ser
596     210                 215                 220
```

```
RAW SEQUENCE LISTING                      DATE: 07/28/2000
PATENT APPLICATION:  US/09/524,531        TIME: 13:29:08

Input Set : A:\imhof.app.txt
Output Set: N:\CRF3\07282000\I524531.raw

598 Glu Ala Ala His Met Asp Ala Val Glu Leu Asn Val Gly Gly Ile Val
599 225             230             235             240
601 Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Leu Leu Ile Phe Gly
602              245             250             255
604 Val Trp Phe Ala Tyr Ser Arg Gly Tyr Phe Glu Thr Thr Lys Lys Gly
605             260             265             270
607 Thr Ala Pro Gly Lys Lys Val Ile Tyr Ser Gln Pro Ser Thr Arg Ser
608         275             280             285
610 Glu Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
611     290             295             300
E--> 615 (??)
```

delete

see following page for more error

```
              RAW SEQUENCE LISTING                    DATE: 08/04/2000
              PATENT APPLICATION:  US/09/524,531      TIME: 15:08:32

              Input Set : A:\Pto.amc
              Output Set: N:\CRF3\08042000\I524531.raw

       3 <110> APPLICANT: RMF Dictagene S.A.
       5 <120> TITLE OF INVENTION: Vascular adhesion molecules and modulation of their
       6       function
       8 <130> FILE REFERENCE: rmf6usseqlist
      10 <140> CURRENT APPLICATION NUMBER: 09/524531
      11 <141> CURRENT FILING DATE: 2000-03-13
      13 <150> PRIOR APPLICATION NUMBER: EP 99.200746.8
      14 <151> PRIOR FILING DATE: 1999-03-11
      16 <160> NUMBER OF SEQ ID NOS: 21
      18 <170> SOFTWARE: PatentIn Ver. 2.1
      20 <210> SEQ ID NO: 1
      21 <211> LENGTH: 20
      22 <212> TYPE: DNA
      23 <213> ORGANISM: Artificial Sequence
      25 <220> FEATURE:
      26 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
      28 <400> SEQUENCE: 1
W--> 29 tayagntgyn nngcytcyaa          see item 10 on Error              20
      32 <210> SEQ ID NO: 2                    Summary Sheet
      33 <211> LENGTH: 20
      34 <212> TYPE: DNA
      35 <213> ORGANISM: Artificial Sequence
      37 <220> FEATURE:
      38 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
      40 <400> SEQUENCE: 2
W--> 41 taycrgtgyn nngcytcyaa   item 10                                  20
      44 <210> SEQ ID NO: 3
      45 <211> LENGTH: 20
      46 <212> TYPE: DNA
      47 <213> ORGANISM: Artificial Sequence
      49 <220> FEATURE:
      50 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
      52 <400> SEQUENCE: 3
W--> 53 taytaytgyn nngcytcyaa   item 10                                  20
      56 <210> SEQ ID NO: 4
      57 <211> LENGTH: 18
      58 <212> TYPE: DNA
      59 <213> ORGANISM: Artificial Sequence
      61 <220> FEATURE:
      62 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
      64 <400> SEQUENCE: 4
      65 gaggtacttg catgtgct                                             18
      68 <210> SEQ ID NO: 5
      69 <211> LENGTH: 19
      70 <212> TYPE: DNA
      71 <213> ORGANISM: Artificial Sequence
      73 <220> FEATURE:
```

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY   DATE: 07/28/2000
PATENT APPLICATION: US/09/524,531   TIME: 13:29:09

Input Set : A:\imhof.app.txt
Output Set: N:\CRF3\07282000\I524531.raw

```
L:29  M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:29  M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:29  M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
L:41  M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:41  M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:41  M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2
L:53  M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:53  M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:53  M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:3
L:513 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:18
L:513 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:18
L:513 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:18
L:529 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:19
L:529 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:19
L:529 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:19
L:545 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:20
L:545 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:20
L:545 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:20
L:615 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:615 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
```